Amendments to the Specification:

Please replace the paragraph beginning at page 8, line 27, with the following rewritten paragraph:

--Figure 19 shows the sequences of SEQ ID NOS:5-16 which represent the primers and probes that were used with the ~~Taqman~~ TAQMAN® analysis.

Please replace the paragraph beginning at page 14, line 15, with the following rewritten paragraph:

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described above using the ALIGN-2 sequence comparison computer program. However, % amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from the NCBI website ~~http://www.ncbi.nlm.nih.gov~~ or otherwise obtained from the National Institutes of Health, Bethesda, MD, USA 20892. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

Please replace the paragraph beginning at page 17, line 9, with the following rewritten paragraph:

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described above using the ALIGN-2 sequence comparison computer program. However, % nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from the NCBI website

~~http://www.ncbi.nlm.nih.gov.~~ or otherwise obtained from the National Institutes of Health, Bethesda, MD USA 20892. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

Please replace the paragraph beginning at page 68, line 27, with the following rewritten paragraph:

–*Inhalation Challenges*: After sensitization and boost, four DMA inhalation challenges were administered starting on day 16. For aerosolization, the final concentration of dust mite in the nebulizer was 6000 units/ml after being diluted with Dulbecco's PBS and 0.1% of ~~Tween®~~ TWEEN®-20. All inhalation challenges were administered in a ~~Plexiglas®~~ PLEXIGLAS® pie exposure chamber. DMA was aerosolized for 20 minutes using a PARI IS-2 nebulizer initially and then refilled with 1.5 ml, 10 minutes into the exposure. Total deposited dose in the lung was ~ 6.5 AU of DMA.–

Please replace the paragraph beginning at page 68, line 32, with the following rewritten paragraph:

AHR (paralyzed): On day 24, approximately 18 hours after the last DMA aerosol challenge the mice were anesthetized with a mixture of pentobarbital (25 mg/kg) and urethane (1.8 g/kg) and catheterized with a 1 cm incision over the right jugular vein. The jugular vein was dissected free and a catheter (PE-10 connected to PE-50) was inserted and tied into place. Additionally, the mice were tracheotomized (1 cm neck incision, trachea dissected free and a cannula inserted and tied into place). The mice were then loaded into a ~~Plexiglas®~~ PLEXIGLAS® flow plethysmograph for measurement of thoracic expansion and airway pressure. The mice were ventilated using 100% oxygen at a frequency of 170 bpm and Vt equal to 9 µl/gm. Breathing mechanics (lung resistance and dynamic compliance) were continuously monitored

using a computerized (Buxco Electronics) data acquisition program. After baseline measurements, the mice received a one-time 10-second dose of the methacholine (MCH dose of 500 μg/kg) using 200 μg/ml MCH as the stock concentration.

Please replace the paragraph beginning at page 69, line 4, with the following rewritten paragraph:

--*Sacrifice*: After completion of the airway reactivity measurement EDTA tubes were used to collect blood via the retro-orbital sinus to obtain serum. The abdomen was opened, the descending aorta severed and the diaphragm cut. After time elapsed for the animals to exsanguinate, bronchioalveolar lavage (BAL) was performed. The lungs were lavaged three times with the same bolus of sterile saline (30 μg/g mouse weight) through the previously inserted tracheal cannula. The bolus filled the lung to approximately 70% total lung capacity. The samples of BAL (return averaged 80%) were centrifuged at 1000 x *g* and 4°C for 10 minutes. The supernatants were decanted and immediately frozen at -80°C. The cell pellets were resuspended in 250 ml of PBS with 2% BSA (Sigman, St. Louis, MO), then enumerated using an automated counter (Baker Instruments, Allentown, PA), and recorded as total number of BAL cells/μl. The cell suspension was then adjusted to 200 cells/μl and 100 ml was centrifuged onto coated ~~Superfrost Plus~~ SUPERFROST PLUS™ microscope slides (Baxter Diagnostics, Deerfield, IL) at 800 x *g* for 10 minutes using a cytospin (Shandon, Inc., Pittsburgh, PA). Slides were air dried, fixed for 1 minute in 100% methanol, and stained with ~~Diff-Quik™~~ DIFF-QUIK™ (Baxter Health Care, Miami, FL). At least 200 cells were evaluated per slide to obtain a differential leukocyte count.--

Please replace the paragraph beginning at page 72, line 37, with the following rewritten paragraph:

--Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents ~~Superfect®~~ SUPERFECT® (Quiagen), ~~Dosper®~~ DOSPER® or ~~Fugene®~~ FUGENE® (Boehringer Mannheim). The cells are

grown as described in Lucas *et al., supra*. Approximately 3 x 10^{-7} cells are frozen in an ampule for further growth and production as described below.--

Please replace the paragraph beginning at page 74, line 21, with the following rewritten paragraph:

--Recombinant baculovirus is generated by co-transfecting the above plasmid and ~~BaculoGold™~~ BACULOGOLD™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley *et al., Baculovirus expression vectors: A Laboratory Manual*, Oxford: Oxford University Press (1994).--

Please replace the paragraph beginning at page 75, line 20, with the following rewritten paragraph:

--Hi5 cells are grown to a confluency of 50% under the conditions of 27°C, no CO_2, no pen/strep. For each 150 mm plate, 30 µg of pIE based vector containing the sequence was mixed with 1 ml ~~Ex-Cell~~ EX-CELL™ medium (Media: ~~Ex-Cell~~ EX-CELL™ 401 + 1/100 L-Glu JRH Biosciences #14401-78P (note: this media is light sensitive)). Separately, 100 µl of ~~Cell Fectin~~ CELLFECTIN™ (~~CellFECTIN~~ CELLFECTIN™, Gibco BRL +10362-010, pre-vortexed) is mixed with 1 ml of ~~Ex-Cell~~ EX-CELL™ medium. The two solutions are combined and incubated at room temperature for 15 minutes. 8 ml of ~~Ex-Cell~~ EX-CELL™ media is added to the 2 ml of DNA/~~CellFECTIN~~ CELLFECTIN™ mix and this is layered on Hi5 cells that have been washed once with ~~Ex-Cell~~ EX-CELL™ media. The plate is then incubated in darkness for 1 hour at room temperature. The DNA/~~CellFECTIN~~ CELLFECTIN™ mix is then aspirated, and the cells are washed once with ~~Ex-Cell~~ EX-CELL™ to remove excess ~~Cell FECTIN~~ CELLFECTIN™. 30 ml of fresh ~~Ex-Cell~~ EX-CELL™ media is added and the cells are incubated for 3 days at 28°C. The supernatant is harvested and the expression of the sequence in the baculovirus expression vector is determined by batch binding of 1 ml of supernatant to 25 ml

of Ni-NTA beads (QIAGEN) for histidine tagged proteins of Protein-A ~~Sepharose~~ SEPHAROSE™ CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.--